Population structure using mtDNA

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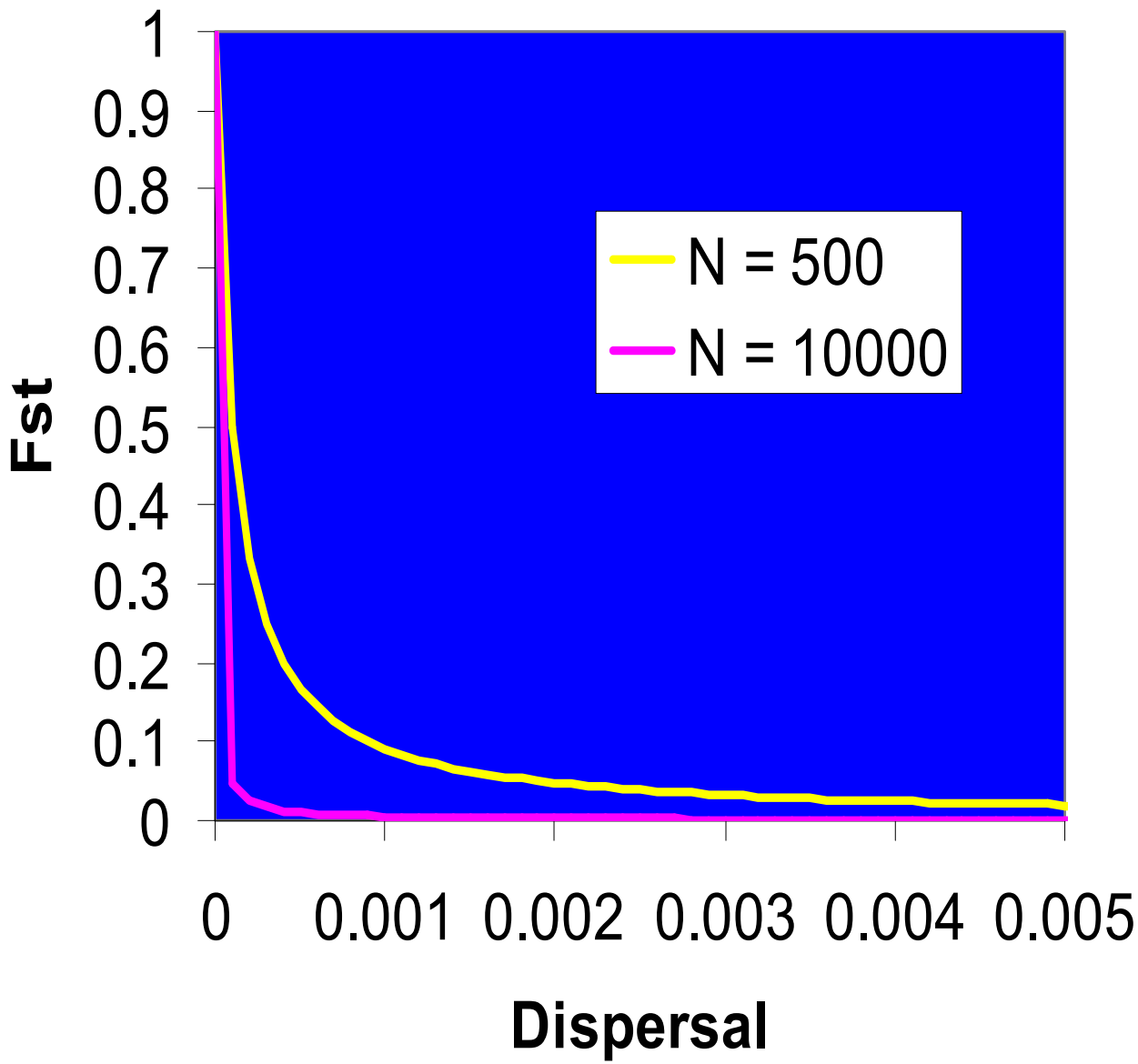
- joint research: SWFSC, NMML, TAMU
- study 2001-107

Study design to estimate dispersal rates

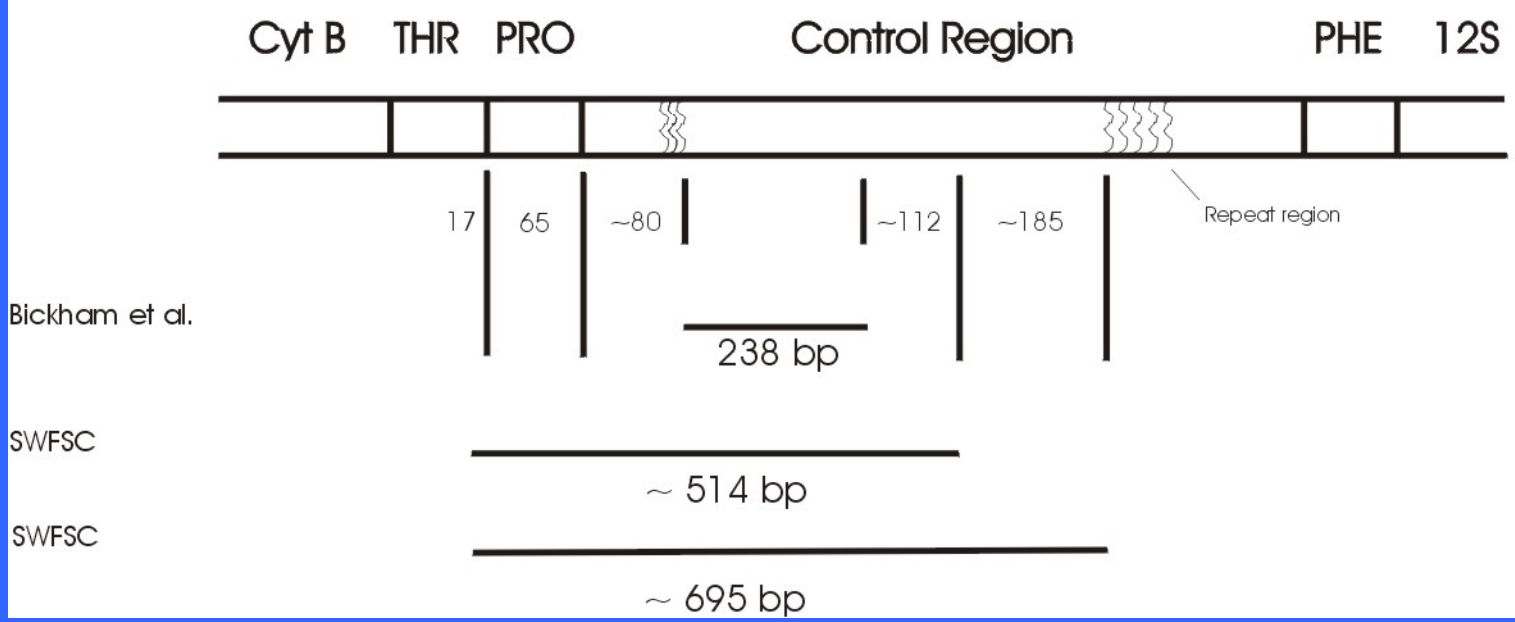
- Level of genetic differentiation between rookeries is expected to be low even for demographically trivial dispersal rates because abundance was high


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Fst
N = 500
N = 10000
0
0.001
0.002
0.003
0.004
0.005
Dispersal

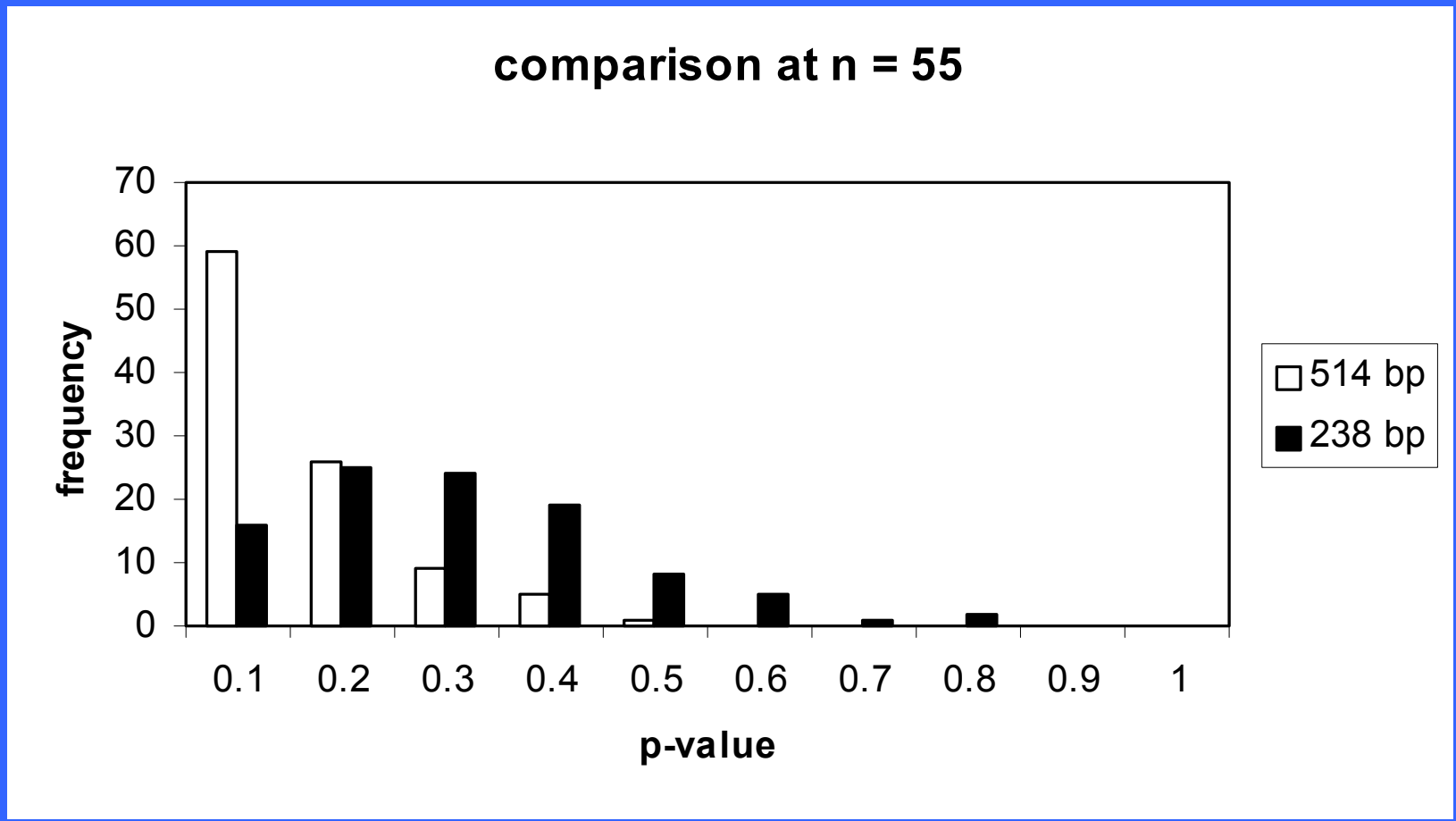
Increase precision by

- increasing the length of mtDNA sequence examined
- increasing sample size to achieve high statistical power

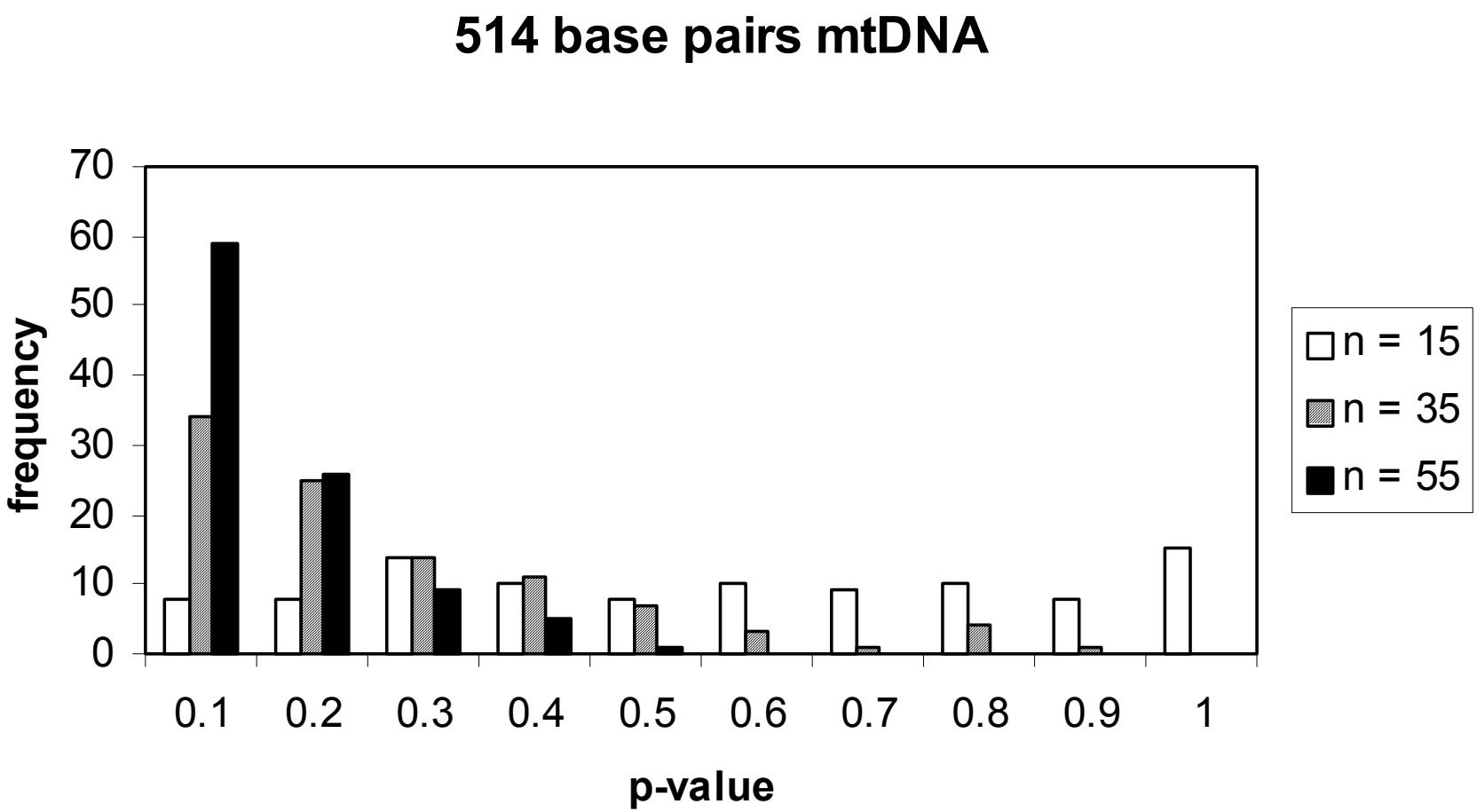
Steller Sea lion, *Eumetopias jubatus*, mtDNA Sequencing



Increasing sequence length increases power



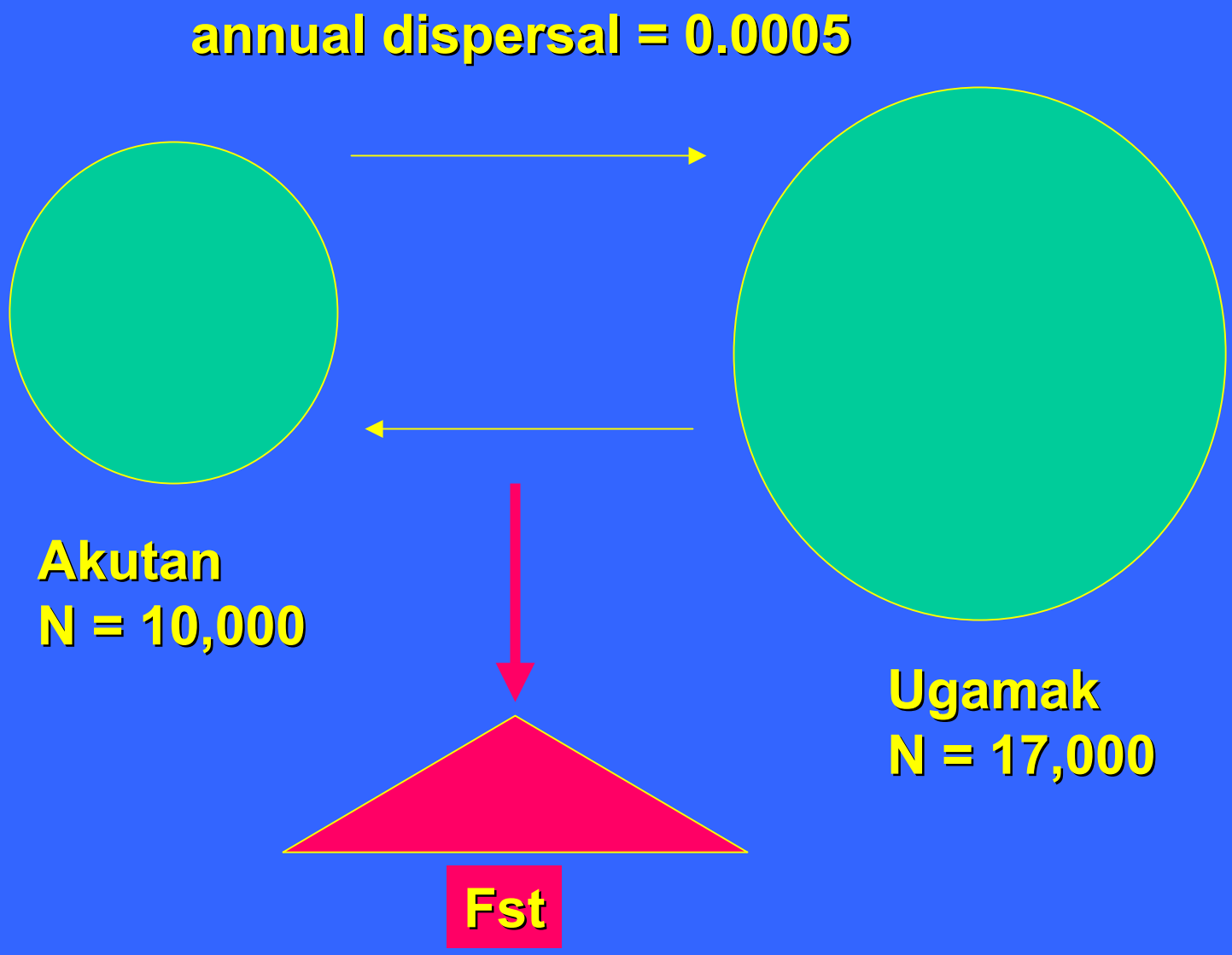
Sample size required >50/rookery

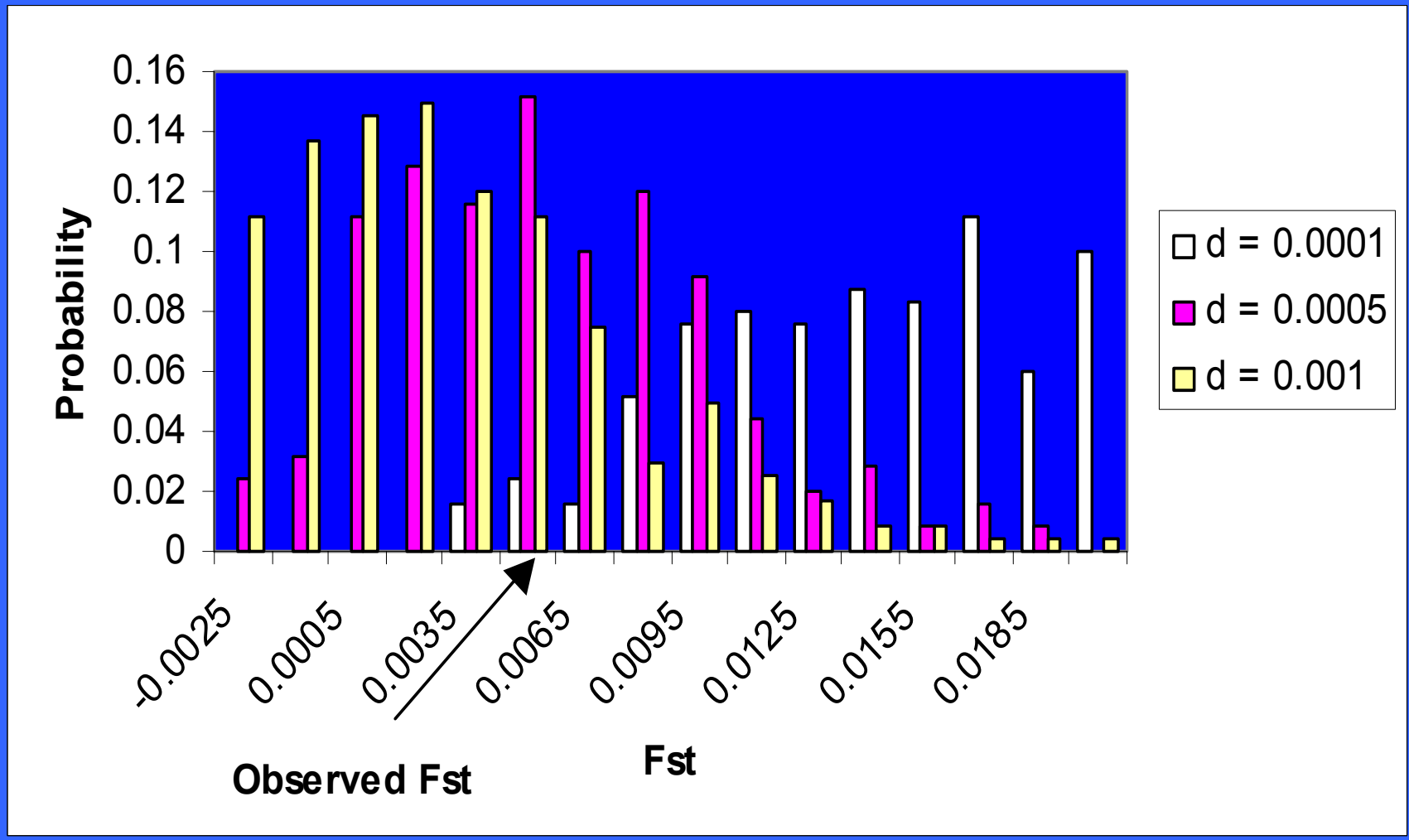


Hypothesis testing results using
Akutan n = 65
Ugamak n = 77

- χ^2 p-value
  - –238 base pairs p = 0.16
  - –514 base pairs p = 0.02

Case specific simulation approach to estimating dispersal





d = 0.0005 is consistent with about 6 females (out of 27,000) moving between these two rookeries

Preliminary conclusions

- there is population structure between adjacent rookeries that is statisically significant
- dispersal estimates are demographically trivial and therefore important for risk assessment
- dispersal estimates at this level are not consistent with DPS status

Recommendations

- extending the length of sequence used is critical for detecting population structure at the demographic level
- **at least 50** samples should be gathered from each rookery to be able to estimate dispersal rates